COBALT

Constraint-based Multiple Alignment Tool

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- Cobalt RID PFMGBSYM212 (4 seqs)

▽ Graphical Overview

⟲	1 - 1,281 (1,281r shown)	Find:	◀ ▶ 🔍 ▭▭▭▭ 🔍 ⚞	⚒ Tools ▾ ⊞ Columns ▾ Rows ▾ ⬇ Download ▾ 🎨 Coloring ▾ ⟳ ▾

Sequence ID	Start		1	1000	1281	End	Organism
QVN46559.1	1					1,254	Bat SARS-like coronavirus
QVN46569.1	1					1,253	Bat SARS-like coronavirus
YP_003858584.1	1					1,259	Bat coronavirus BM48-31/
BCA87361.1	1					1,273	Severe acute respiratory s

PROTEIN: 1 - 1,281 (1,281r shown)   ✎ ⚙ Rows shown: 4/4
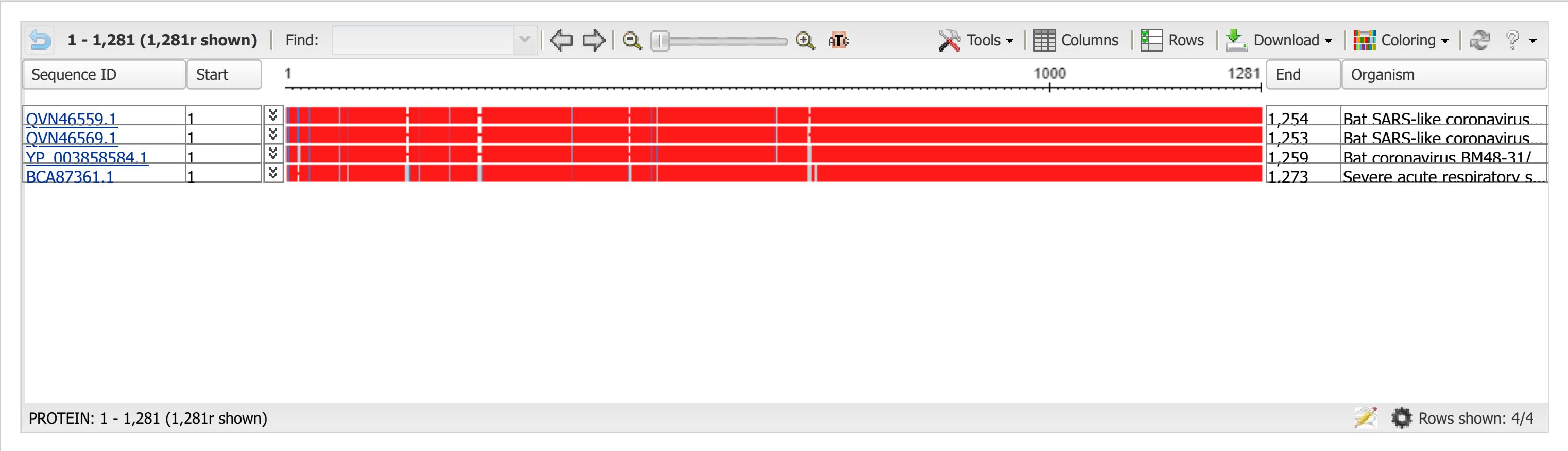
▽ Descriptions   ☑ Select All   Re-align   ▷Alignment parameters

Accession	Description	Links
☑ QVN46559.1	spike glycoprotein [Bat SARS-like coronavirus Khosta-1]	
☑ QVN46569.1	spike glycoprotein [Bat SARS-like coronavirus Khosta-2]	
☑ YP_003858584.1	spike protein [Bat coronavirus BM48-31/BGR/2008]	Related Information
☑ BCA87361.1	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	

▽ Alignments   ☑ Select All   Re-align   Mouse over the sequence identifer for sequence title

View Format: Expanded ▾   ⓘ   Conservation Setting: 2 Bits ▾   ⓘ

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☑ QVN46559.1       1   MKFFIFLSFLPLITAQEG-CGVLSNKSTPNLDQFLSSRRGFYYFDDTFRSSVRVLTSGYFLPFQSNLTRYLTLESITGRR   79
☑ QVN46569.1       1   MKLFLFLFLLPLVGAQDG-CATLSTKLTPTQLQVNSTRRGFYYFDDIYRSSLRVLVPGYFLPFGTNITRYQA-QVINWTA   78
☑ YP_003858584.1   1   MKFLAFLCLLGFANAQDGkCGTLSNKSPSKLTQTPSSRRGFYYFDDIFRSSIRVLTTGHFLPFNTNLTWYLTLKSNGKQR   80
☑ BCA87361.1       1   --MFVFLVLLPLVSSQ---CVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG   75

☑ QVN46559.1      80   IY-FDNPNIPFKDGLYFAATEKSNVIRGWIFGSTLDNTTQSAVLFNNGTHIVVNVCNFNFCQDPMLAISAGSPYKSW---  155
☑ QVN46569.1      79   IF-FDNPVIPFNDGVYFAALEHSNVVRGWIFGTTLDNTTQSAIVVNNATHILISVCYFNVCKEPMFAVSNFKPYKSW---  154
☑ YP_003858584.1  81   IY-YDNPNINFGDGVYFGLTEKSNVFRGWIFGSTLDNTTQSAVLFNNGTHIVIDVCNFNFCADPMFAVNSGQPYKTW---  156
☑ BCA87361.1      76   TKrFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWmes  155

☑ QVN46559.1     156   ---VYTTATNCTYNRL-HAFNISTSINPGSFVHLREHVFRNVDGFLYVYHNYESINVTNTFPGGFSVLKPILKLPFGLNI  231
☑ QVN46569.1     155   ---VYDRANNCTFNRA-YPLNISTTPEPGKFKALREQVFRYQDGFLYIYHSYESIN-SDTLPPGFSVLKPMLKLPLGLNI  229
☑ YP_003858584.1 157   ---IYTSAANCTYHRA-HAFNISTNMNPGKFKHFREHLFKNVDGFLYVYHNYEPIDLNSGFPSGFSVLKPILKLPFGLNI  232
☑ BCA87361.1     156   efrVYSSANNCTFEYVsQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINI  235

☑ QVN46559.1     232   THFKVIMTLFSN------TTQSFEADASAYFVGHLKPLTMLADFDENGTIVDAVDCSQNPLSELKCTTKSFSVEKGIYQT  305
☑ QVN46569.1     230   TRFRVVMAMHSL------TTSNFNTHSVNYFVGHLKPLTMLVEFSPNGTIIDAIDCSQDPLSELKCTTKSFSVEKGIYQT  303
☑ YP_003858584.1 233   TVVKAIMTLFSS------TQSNFDADASAYFVGHLKPLTMLVDFDENGTIIDAIDCSQDPLSELKCTTKSFTVEKGIYQT  306
☑ BCA87361.1     236   TRFQTLLALHRSyltpgdSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT  315

☑ QVN46559.1     306   SNFRVSPSTEVVRFPNITNLCPFGQVFNASTFPSVYAWGRMRISDCVADYSVLYNSTSSFSTFKCYGVSPTKLNDLCFSS  385
☑ QVN46569.1     304   SNFRVSPSLDVVRFPNMTNICPFDQVFNKTQFPSVYAWERVRISDCVSDYTVLYNSSASFSTFKCYGVSPTKLNDLCFSG  383
☑ YP_003858584.1 307   SNFRVTPTTEVVRFPNITQLCPFNEVFNITSFPSVYAWERMRITNCVADYSVLYNSSASFSTFQCYGVSPTKLNDLCFSS  386
☑ BCA87361.1     316   SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNS-ASFSTFKCYGVSPTKLNDLCFTN  394

☑ QVN46559.1     386   VYADYFVVKGDDVRQIAPAQTGVIADYNYKLPDDFTGCVLAWNTKSIDKG----QGFYYRLFRHGKIKPYERDTSNVPYN  461
☑ QVN46569.1     384   VYADYFVVKGDHVHQIAPGQTGVIADYNYKLPSEFVGCILAWNTRTIDSK----RGFYYRLFRHGNIRPYERDTSNVPYN  459
☑ YP_003858584.1 387   VYADYFVVKGDDVRQIAPAQTGVIADYNYKLPDDFTGCVIAWNSNNLDSS----NEFFYRRFRHGKIKPYGRDLSNVLFN  462
☑ BCA87361.1     395   VYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKvggnYNYLYRLFRKSNLKPFERDISTEIYQ  474

☑ QVN46559.1     462   AQGGTCTDTSQLNCYQPLKSYDFTDTVGVGYQPYRVVVLSFELLNAPATVCGPKQSTELVKNKCVNFNFNGLTGTGVLTE  541
☑ QVN46569.1     460   AAGGTCNQPGTHNCYEPLQDYGFTSTSGVGYQPFRVVVLSFELLNAPATVCGPKQSTDLVKNKCVNFNFNGLTGTGVLTD  539
☑ YP_003858584.1 463   PSGGTCS-AEGLNCYKPLASYGFTQSSGIGFQPYRVVVLSFELLNAPATVCGPKQSTELVKNKCVNFNFNGLTGTGVLTN  541
☑ BCA87361.1     475   AGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTE  554

☑ QVN46559.1     542   STKRFQSFQQFGRDISDFTDSVRDPKTLEILDISPCSYGGVSVITPGTNASNVVAVLYQDVNCTDVPTMLHTEQVAHDWR  621
☑ QVN46569.1     540   SNKKFQPFQQFGRDSADFTDSVKDPKTLEILDITPCSYGGVSVITPGTNTSDSVAVLYQDVNCTDVPTMLHMDQVSNDWR  619
☑ YP_003858584.1 542   STKKFQPFQQFGRDVSDFTDSVRDPKTLEILDIAPCSYGGVSVITPGTNASSSVAVLYQDVNCTDVPTMLHADQISHDWR  621
☑ BCA87361.1     555   SNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWR  634

☑ QVN46559.1     622   VYAVNTDGNMFQTQAGCLVGATYENTSYECDIPIGAGVCAKFGST-----KTRQ---QSILAYTMSIGEDQSVAYSNNSI  693
☑ QVN46569.1     620   VYAVNTDGNMFQTQAGCLVGATYDNTSYECDIPVGAGVCAKFQTTT----RAKQ---SSILAYTMSLGEDSNVAYSNNSI  692
☑ YP_003858584.1 622   VYAFRNDGNIFQTQAGCLIGAAYDNSSYECDIPIGAGICAKYTNVSSTLVRSGG---HSILAYTMSLGDNQDIVYSNNTI  698
☑ BCA87361.1     635   VYS--TGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARsvasQSIIAYTMSLGAENSVAYSNNSI  712

☑ QVN46559.1     694   AIPTNFSISVTTEVLPVSMTKTSVDCNMYICGDSTECSNLLLQYGSFCTQLNRALSGIAVEQDRNTRDVFAQTKTIYKTP  773
☑ QVN46569.1     693   AIPTNFTISVTTEVLPVSMTKTAVDCNMYICGDSTECSSLLLQYGSFCQQLNRALAGVSVEQDKNTQDVFAQVKSIYKVS  772
☑ YP_003858584.1 699   AIPMNFSISVTTEVLPVSMTKTSVDCNMYICGDSTECSNLLLQYGSFCTQLNRALAGIAVEQDRNTRDVFAQTKAMVKTP  778
☑ BCA87361.1     713   AIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTP  792

☑ QVN46559.1     774   NIKDFGGFNFSQILPDPGKPSQRSFIEDLLYNKVTLADPGFMKQYGDCLGGINARDLICAQKFNGLTVLPPLLTDDMIAA  853
☑ QVN46569.1     773   AIKDFGGFNFSQILPDPAKPSKRSFIEDLLYNKVTLADPGFMKQYGDCLGGVNARDLICAQKFNGLTVLPPLLTDDMIAA  852
☑ YP_003858584.1 779   SLKDFGGFNFSQILPDPAKPSSRSFIEDLLFNKVTLADPGFMKQYGDCLGGINARDLICAQKFNGLTVLPPLLTDEMIAA  858
☑ BCA87361.1     793   PIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQ  872

☑ QVN46559.1     854   YTAALISGTATAGYTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQDSLTTTTTALGKLQDVI  933
☑ QVN46569.1     853   YTSALVSGTALSGFTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTTATALGKLQDVI  932
☑ YP_003858584.1 859   YTAALISGTATAGFTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQDSLSTTTTTALGKLQDVI  938
☑ BCA87361.1     873   YTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVV  952

☑ QVN46559.1     934   NQNAAALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSEC  1013
☑ QVN46569.1     933   NQNAIALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAADIRASANLAATKMSEC  1012
☑ YP_003858584.1 939   NQNAIALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSEC  1018
☑ BCA87361.1     953   NQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSEC  1032

☑ QVN46559.1    1014   VLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSEQKNFTTAPAICHNGKAYFPKEGVFVMNGTHWFITQRNFYSP  1093
☑ QVN46569.1    1013   VLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQDKNFTTAPAICHKGKAYFPREGVFVTNGTHWFVTQRNFYQP  1092
☑ YP_003858584.1 1019  VLGQSKRVDFCGKGYHLMSFPQSVYVPSQEQNFTTAPAICHEGKAHFPREGVFVSNGTHWFITQRNFYSP  1098
☑ BCA87361.1    1033   VLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEP  1112

☑ QVN46559.1    1094   QVITTDNTFESGTCDVVIGIVNNTVYDPLQPELESFKQELDKYFKNHTSPDVGLGDISGINASVVDIKKEIEHLNEIAKN  1173
☑ QVN46569.1    1093   EVITTENTFESGNCDVVIGIVNNTVYDPLQPELESFKEELDKYFKNHTSPDVDFDDISGINASVVDIKKEIEHLNEIAKS  1172
☑ YP_003858584.1 1099  QPITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVVSLDGLNNINASVVDIKKEIEHLNEIAKS  1178
☑ BCA87361.1    1113   QIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKN  1192

☑ QVN46559.1    1174   LNESLIDLQELGKYEQYIKWPWYVWLGFIAGIIAIVMATIMLCCMTSCCSCFKGLCSCGSCCKFDEDTSEPVLKGVKLHY  1253
☑ QVN46569.1    1173   LNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIIMATIMLCCMTSCCSCLKGLCSCGSCCKFDDDHSEPVLKGVKLHY  1252
☑ YP_003858584.1 1179  LNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMATIMLCCMTSCCSCLKGVCSCASCCKFDEDDSEPVLTGVKLHY  1258
☑ BCA87361.1    1193   LNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHY  1272

☑ QVN46559.1    1254   T  1254
☑ QVN46569.1    1253   T  1253
☑ YP_003858584.1 1259  T  1259
☑ BCA87361.1    1273   T  1273
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